Amendments to the Specification

Please replace the paragraph spanning pages 5 to 6 of the specification with the following new paragraph.

The application WO 00/60059 discloses variants which have been developed with respect to an altered cleavage pattern on the substrate starch and which are therefore particularly suitable for the processing of starch; for this, according to said application, generating long branched oligosaccharides is more advantageous than generating shorter branched oligosaccharides. Said document discloses numerous point mutations both of native α-amylases and of hybrid amylases, such as, for example, AL33 and AL37 (whose sequences are identical), which, inter alia, may also contain a mutation in position 412 (according to the counting of *B. licheniformis*, SEQ ID NO:2), preferably T412A; in addition to this, however, at least a second mutation must be present in any of positions 13, 48 to 54, 57, 107, 108, 111, 168 and 197; preference is given to multiple mutants with still further substitutions.

Please replace the first full paragraph on page 6 of the specification with the following new paragraph.

None of the last-mentioned three documents discloses, according to numbering of *B. amyloliquefaciens*, SEQ ID NO:4, positions 17, 34 (corresponding to 36 according to the numbering of *B. licheniformis*, SEQ ID NO:2), 76, 108, 112, 142, 147, 149, 151, 163, 174, 179, 185, 191, 198, 207, 231, 234, 244, 256, 263, 276, 431, 84, 99, 429, 201, 19, 433 or 153 as points of fusion. Likewise, no hybrid amylases with sequence variations in positions 134 or 320 (counting according to *B. licheniformis*, SEQ ID NO:2) are disclosed, and disclosure of a mutation in position 412 took place in combination with further defined variation and in connection with a special change in enzymic activity.

Please replace the paragraph spanning pages 18 to 19 of the specification with the following new paragraph.

The sequences of these two starting enzymes may be obtained from publically accessible databases by the names amyA (for *B. amyloliquefaciens* α-amylase) or amyL (for *B. licheniformis* α-amylase). In the Swiss-Prot database (Geneva Bioinformatics (GeneBio) S.A., Geneva, Switzerland~~; http://www.genebio.com/sprot.html~~), for example, they are listed under the accession numbers P00692 (for *B. amyloliquefaciens* α-amylase amyA) and P06278 (for *B. licheniformis* α-amylase amyL). In addition, they are indicated in the sequence listing of the present application under SEQ ID No. 4 and SEQ ID No. 2, respectively; together with the corresponding nucleotide sequences under SEQ ID No. 3 and SEQ ID No. 1, respectively.

Please replace the first full paragraph on page 19 of the specification with the following new paragraph.

Both Bacillus species have been described in detail in the literature and are also generally accessible via strain collections. Thus, for example, *B. amyloliquefaciens* is obtainable under the name DSM 7 from the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, 38124 Braunschweig, Germany ~~(http://www.dsmz.de)~~ or under the name ATCC 23350 from the American Type Culture Collection, 10801 University Boulevard, Manassas, VA 20110-2209, USA ~~(http://www.atcc.org)~~. *B licheniformis* may be obtained from the same sites, for example under the names DSM 13, and ATCC 14580, respectively.

Please replace the first full paragraph on page 20 of the specification with the following new paragraph.

Additional numbers characterize the molecule unambiguously with respect to the site at which, i.e. to the amino acid C-terminally from which, fusion has taken place. If in doubt, the counting of *B. amyloliquefaciens* α-amylase (SEQ ID No. 4) is definitive. Thus, for example, the molecule AL76 has the N-terminal 76 amino acids of *B. amyloliquefaciens* amylase and, adjacent thereto down to the C-terminus, the homologous amino acids of *B. licheniformis* α-amylase, i.e. from the tyrosine present in position 79, according to the numbering of *B. licheniformis* α-amylase (SEQ ID NO:2). The hybrid amylase LAL19-433, for example,

consists of the N-terminal 21 amino acids of *B. licheniformis* α-amylase, followed by the homologous region of *B. amyloliquefaciens* α-amylase, i.e. starting with the tryptophan which follows the histidine in homologous complementation down to the glycine which corresponds to position 433 according to both countings, and finally of the remaining amino acids of *B. licheniformis* α-amylase, i.e. the region of amino acids 434 to 483. The points of fusion are also highlighted in figure 2.